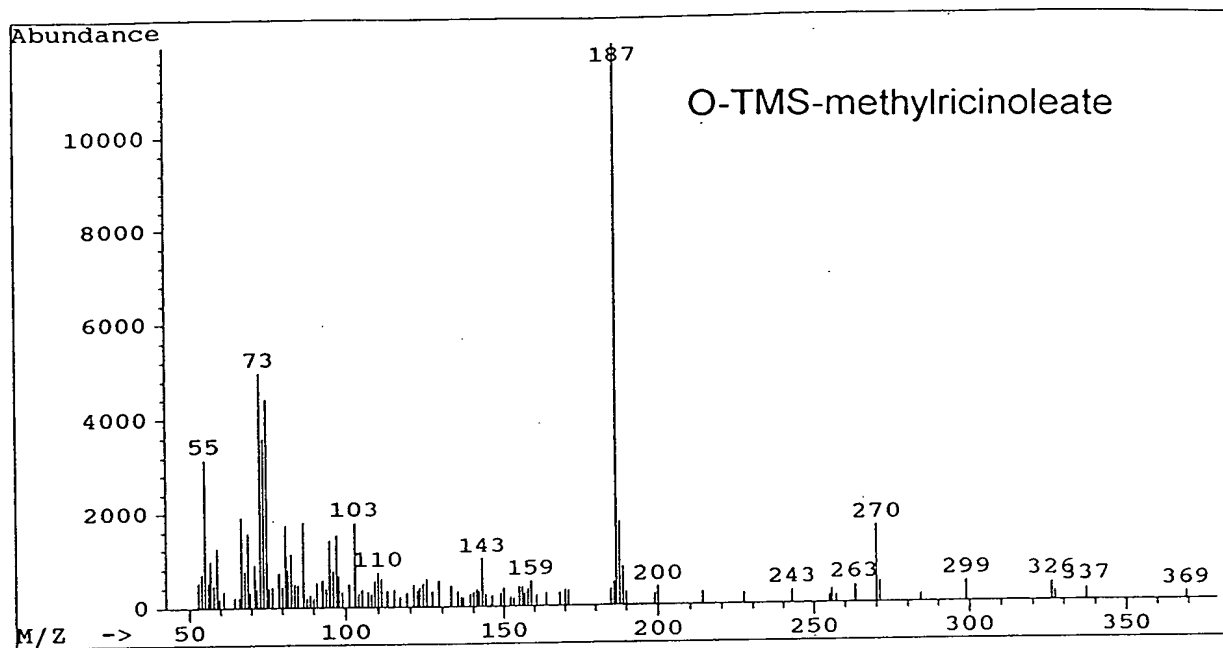
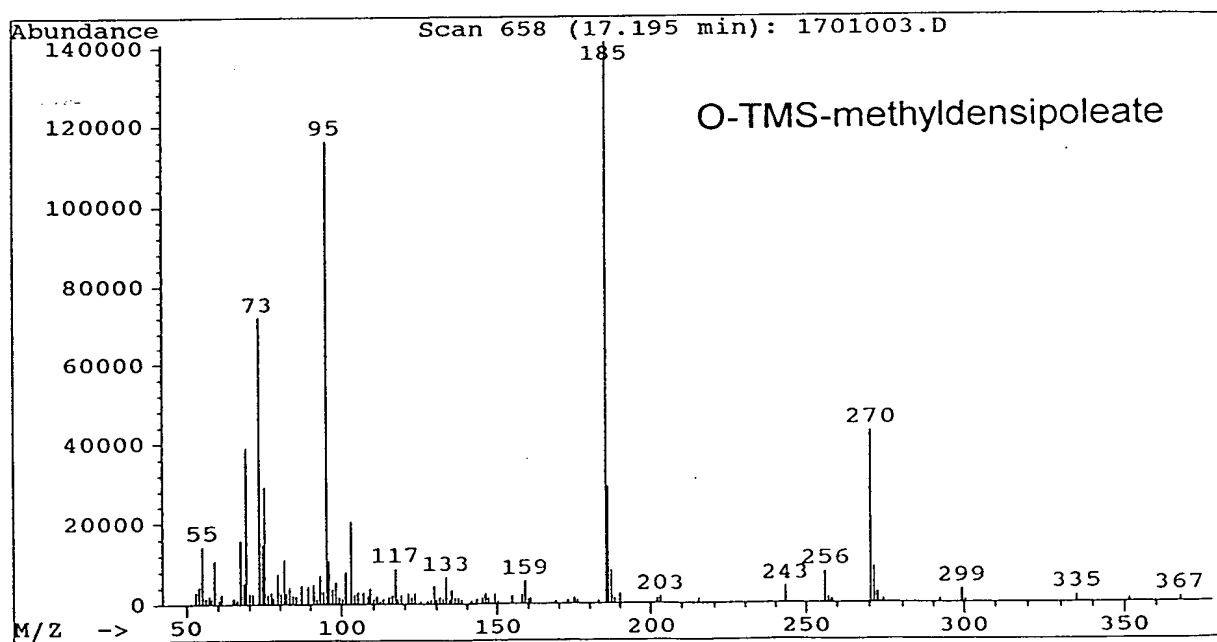


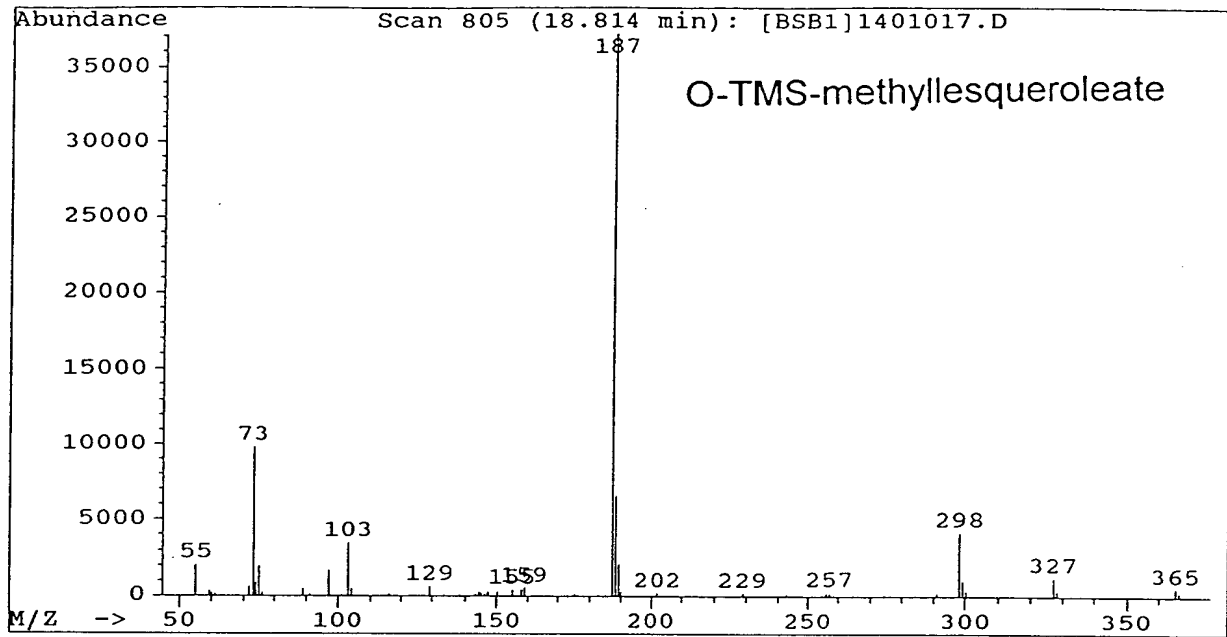
Figure 1A



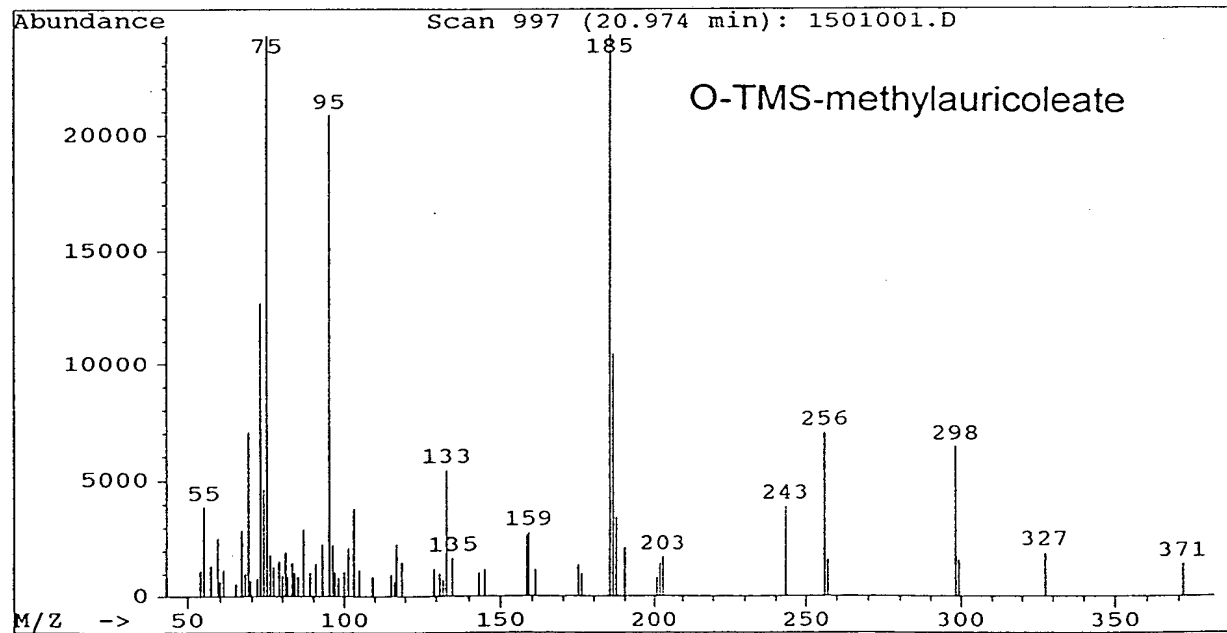
1B



1C



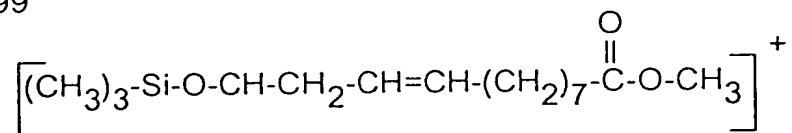
1D



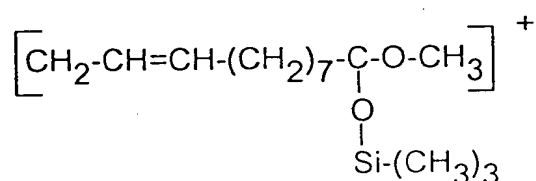
0005189-06101  
101290-6815860

Ion #1: Mass 187  $\left[ \text{CH}_3-(\text{CH}_2)_5-\text{CH}-\text{O}-\text{Si}-(\text{CH}_3)_3 \right]^+$

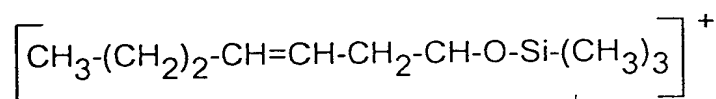
Ion #2: Mass 299



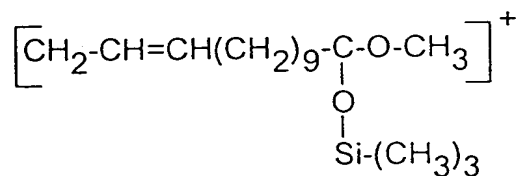
Ion #3: Mass 270 (characteristic rearrangement ion)



Ion #4: Mass 185 (desaturated analog of Ion #1)



Ion #5: Mass 298 (elongated analog of Ion #3)



Ion #6: Mass 327 (elongated analog of ion

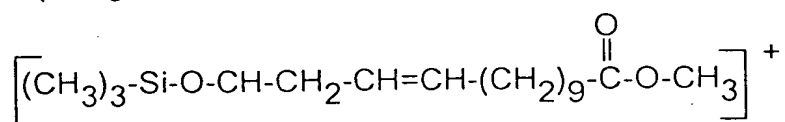


Figure 2

Figure 3

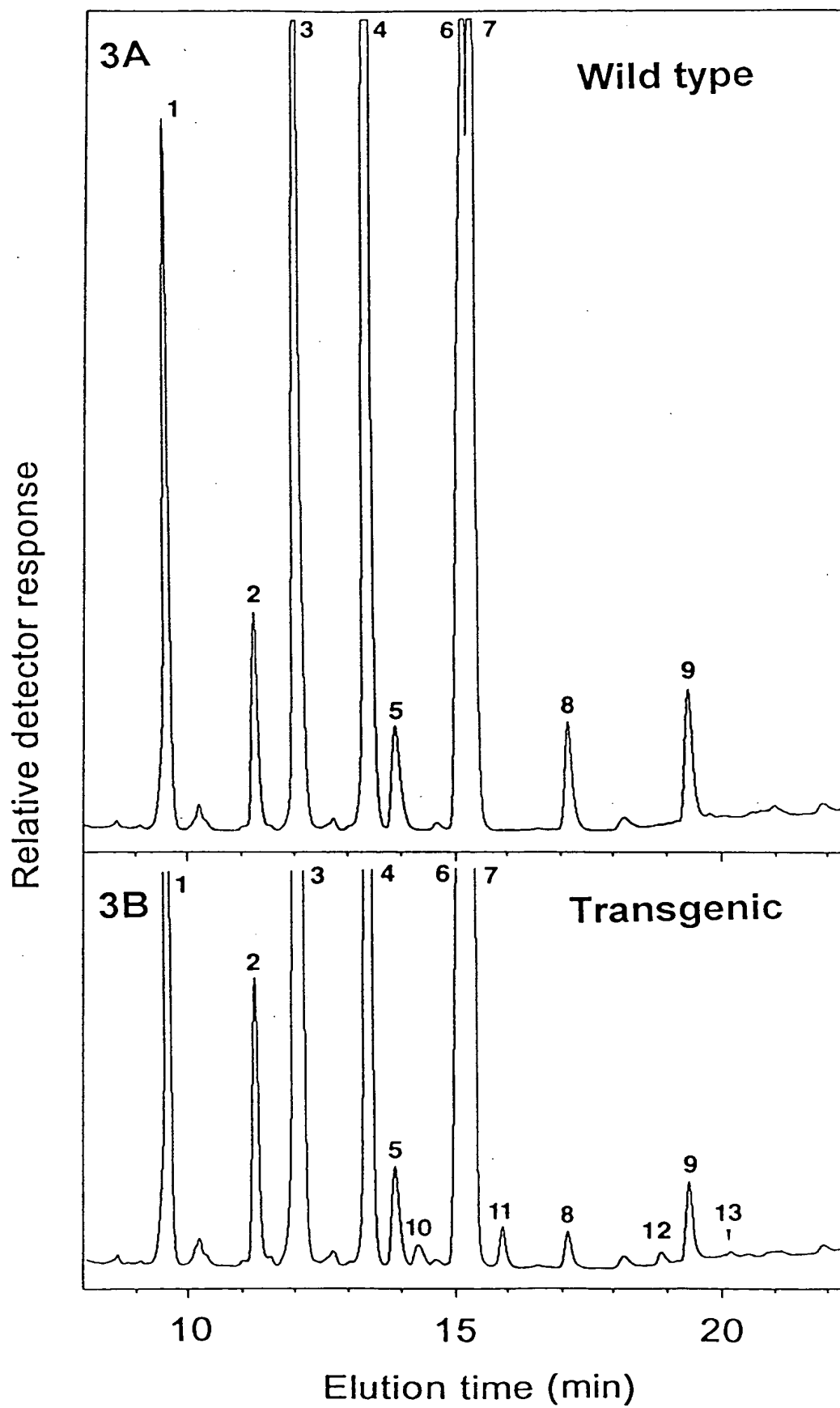
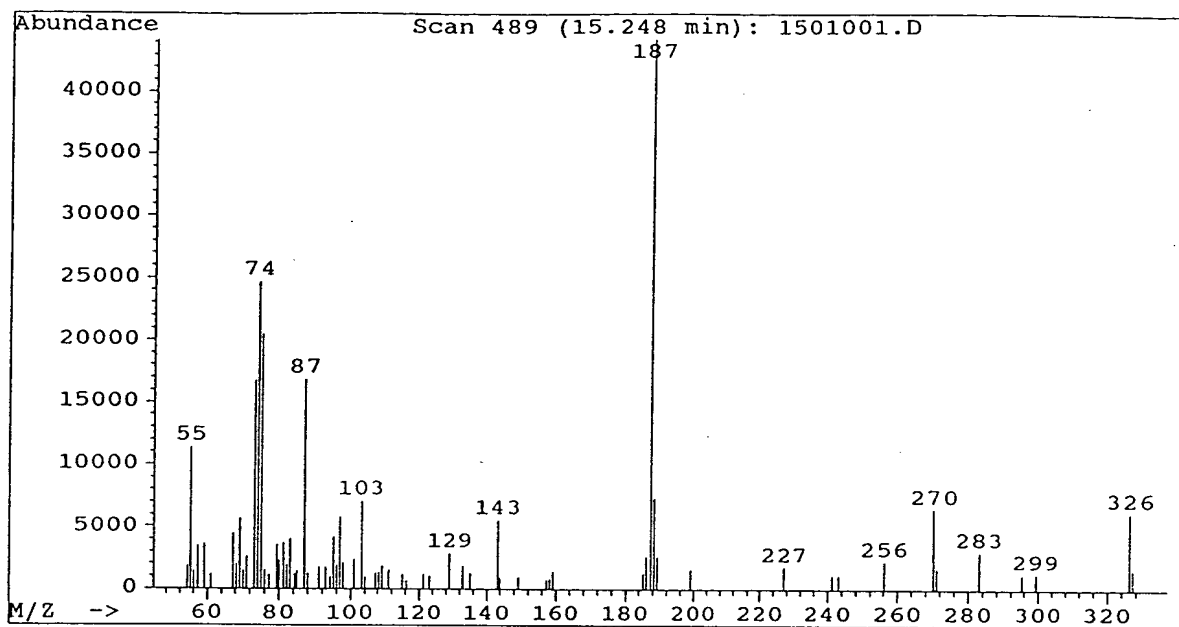
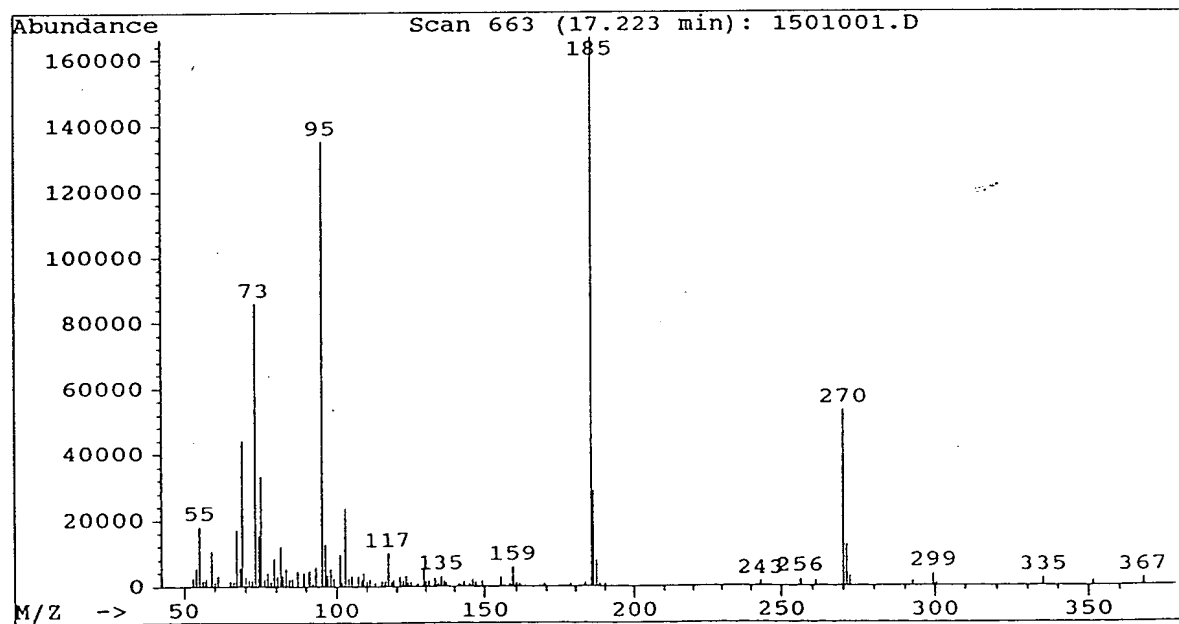


Figure 4A Mass spectrum of peak 10 from figure 3B



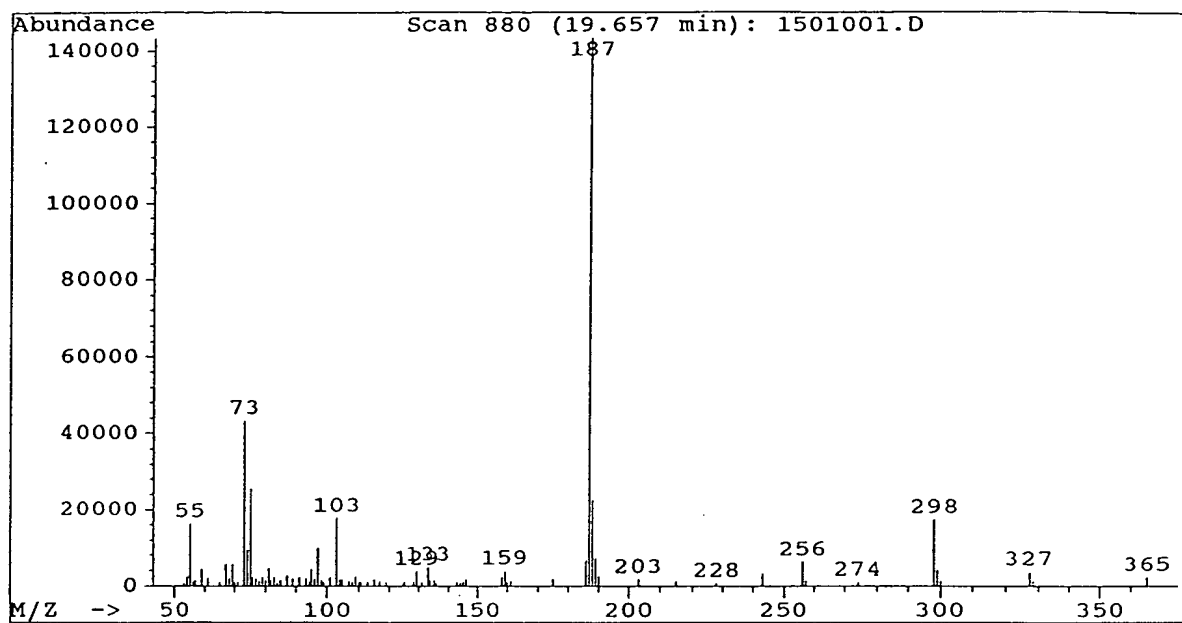
4B Mass spectrum of peak 11 from figure 3B



0985189 062101  
TOT290 66T58860

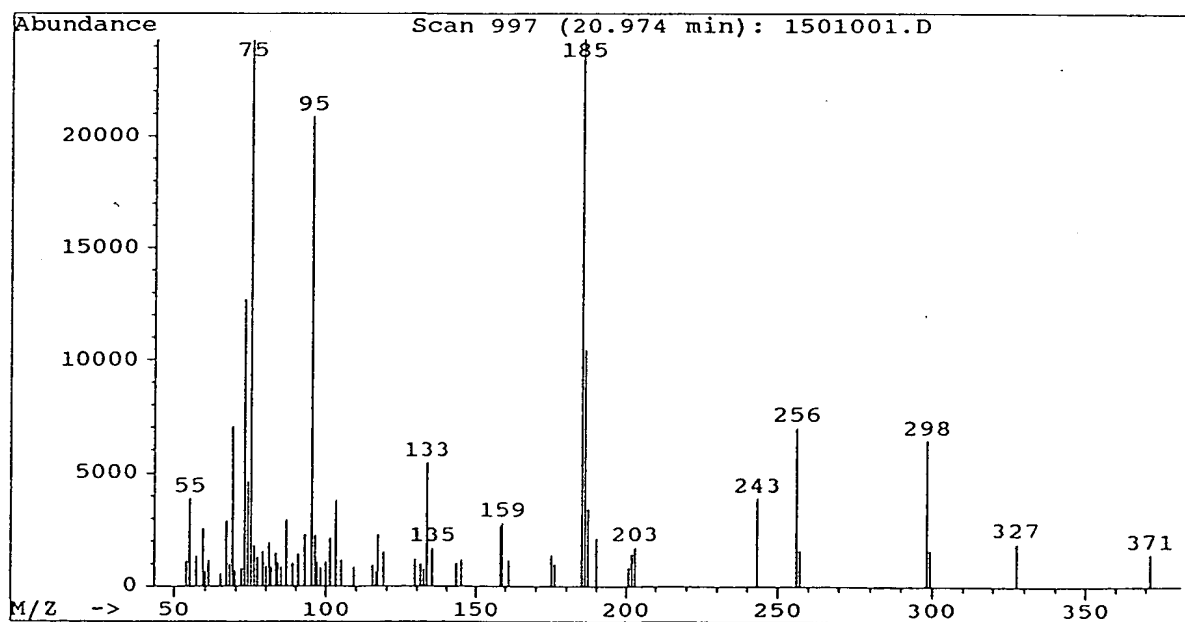
4C

## Mass spectrum of peak 12 from figure 3B



4D

## Mass spectrum of peak 13 from figure 3B



0985189-052101

10	20	30	40	50	60
TATTGGCACC	GGCGGCACCA	TTCCAACAAT	GGATCCCTAG	AAAAAGATGA	AGTCTTTGTC
70	80	90	100	110	120
CCACCTAAGA	AAGCTGCAGT	CANATGGTAT	GTCAAATACC	TCAACAACCC	TCTTGGACGC
130	140	150	160	170	180
ATTCTGGTGT	TAACAGTTCA	GTTTATCCTC	GGGTGGCCTT	TGTATCTAGC	CTTTAATGTA
190	200	210	220	230	240
TCAGGTAGAC	CTTATGATGG	TTTCGCTTCA	CATTTCTTCC	CTCATGCACC	TATCTTTAAG
250	260	270	280	290	300
GACCGTGAAC	GTCTCCAGAT	ATACATCTCA	GATGCTGGTA	TTCTAGCTGT	CTGTTATGGT
310	320	330	340	350	360
CTTTACCGTT	ACGCTGCTTC	ACAAGGATTG	ACTGCTATGA	TCTGCGTCTA	CGGAGTACCG
370	380	390	400	410	420
CTTTTGATAG	TGAACTTTTT	CCTTGTCTTG	GTCACTTTCT	TGCAGCACAC	TCATCCTTCA
430	440	450	460	470	480
TTACCTCACT	ATGATTCAAC	CGAGTGGGAA	TGGATTAGAG	GAGCTTTGGT	TACGGTAGAC
490	500	510	520	530	540
AGAGACTATG	GAATCTTGAA	CAAGGTGTTT	CACAACATAA	CAGACACCCA	CGTAGCACAC
550					
CAC					

Figure 5

10	20	30	40	50	60
TATAGGCACC	GGAGGCACCA	TTCCAACACA	GGATCCCTCG	AAAGAGATGA	AGTATTTGTC
70	80	90	100	110	120
CCAAAGCAGA	AATCCGCAAT	CAAGTGGTAC	GGCGAATACC	TCAACAACCC	TCCTGGTCGC
130	140	150	160	170	180
ATCATGATGT	TAAGTGTCCA	GTTCGTCCTC	GGATGGCCCT	TGTACTTAGC	CTTCAACGTT
190	200	210	220	230	240
TCTGGCAGAC	CCTACAATGG	TTTCGCTTCC	CATTTCTTCC	CCAATGCTCC	TATCTACAAC
250	260	270	280	290	300
GACCGTGAAC	GCCTCCAGAT	TTACATCTCT	GATGCTGGTA	TTCTAGCCGT	CTGTTATGGT
310	320	330	340	350	360
CTTTACCGTT	ACGCTGTTGC	ACAAGGACTA	GCCTCAATGA	TCTGTCTAAA	CGGAGTTCCG
370	380	390	400	410	420
CTTCTGATAG	TTAACTTTTT	CCTCGTCTTG	ATCACTTACT	TACAACACAC	TCACCTGCG
430	440	450	460	470	480
TTGCCTCACT	ATGATTCATC	AGAGTGGGAT	TGGCTTAGAG	GAGCTTTAGC	TACTGTAGAC
490	500	510	520	530	540
AGAGACTATG	GAATCTTGAA	CAAGGTGTTC	CATAACATCA	CAGACACCCA	CGTCGCACAC
550					

CACT

0985189-062101

Figure 6



09885189-062404

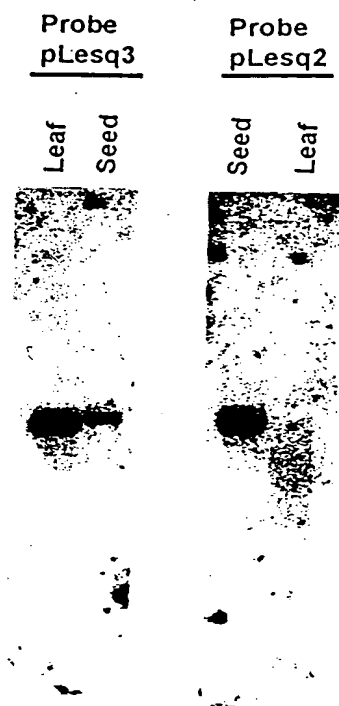


Figure 7

AT GAA GCT TTA TAA GAA GTT AGT TTT CTC TGG TGA CAG AGA AAT TNT	47
GTC AAT TGG TAG TGA CAG TTG AAG CAA CAG GAA CAA CAA GGA TGG TTG	95
GTG NTG ATG CTG ATG TGG TGA TGT GTT ATT CAT CAA ATA CTA AAT ACT	143
ACA TTA CTT GTT GCT GCC TAC TTC TCC TAT TTC CTC CGC CAC CCA TTT	191
TGG ACC CAC GAN CCT TCC ATT TAA ACC CTC TCT CGT GCT ATT CAC CAG	239
AAG AGA AGC CAA GAG AGA GAG AGA GAG AAT GTT CTG AGG ATC ATT GTC	287
TTC TTC ATC GTT ATT AAC GTA AGT TTT TTT TGA CCA CTC ATA TCT AAA	335
ATC TAG TAC ATG CAA TAG ATT AAT GAC TGT TCC TTC TTT TGA TAT TTT	383
CAG CTT CTT GAA TTC AAG ATG GGT GCT GGT GGA AGA ATA ATG GTT ACC	431
Pro Ser Ser Lys Lys Ser Glu Thr Glu Ala Leu Lys Arg Gly Pro Cys	26
CCC TCT TCC AAG AAA TCA GAA ACT GAA GCC CTA AAA CGT GGA CCA TGT	479
Glu Lys Pro Pro Phe Thr Val Lys Asp Leu Lys Lys Ala Ile Pro Gln	42
GAG AAA CCA CCA TTC ACT GTT AAA GAT CTG AAG AAA GCA ATC CCA CAG	527
His Cys Phe Lys Arg Ser Ile Pro Arg Ser Phe Ser Tyr Leu Leu Thr	58
CAT TGT TTC AAG CGC TCT ATC CCT CGT TCT TTC TCC TAC CTT CTC ACA	575
Asp Ile Thr Leu Val Ser Cys Phe Tyr Tyr Val Ala Thr Asn Tyr Phe	74
GAT ATC ACT TTA GTT TCT TGC TTC TAC TAC GTT GCC ACA AAT TAC TTC	623
Ser Leu Leu Pro Gln Pro Leu Ser Thr Tyr Leu Ala Trp Pro Leu Tyr	90
TCT CTT CTT CCT CAG CCT CTC TCT ACT TAC CTA GCT TGG CCT CTC TAT	671
Trp Val Cys Gln Gly Cys Val Leu Thr Gly Ile Trp Val Ile Gly His	106
TGG GTA TGT CAA GGC TGT GTC TTA ACC GGT ATC TGG GTC ATT GGC CAT	719
Glu Cys Gly His His Ala Phe Ser Asp Tyr Gln Trp Val Asp Asp Thr	122
GAA TGT GGT CAC CAT GCA TTC AGT GAC TAT CAA TGG GTA GAT GAC ACT	767
Val Gly Phe Ile Phe His Ser Phe Leu Leu Val Pro Tyr Phe Ser Trp	138
GTT GGT TTT ATC TTC CAT TCC TTC CTT CTC GTC CCT TAC TTC TCC TGG	815
Lys Tyr Ser His Arg Arg His His Ser Asn Asn Gly Ser Leu Glu Lys	154
AAA TAC AGT CAT CGT CGT CAC CAT TCC AAC AAT GGA TCT CTC GAG AAA	863
Asp Glu Val Phe Val Pro Pro Lys Lys Ala Ala Val Lys Trp Tyr Val	170
GAT GAA GTC TTT GTC CCA CCG AAG AAA GCT GCA GTC AAA TGG TAT GTT	911
Lys Tyr Leu Asn Asn Pro Leu Gly Arg Ile Leu Val Leu Thr Val Gln	186
AAA TAC CTC AAC AAC CCT CTT GGA CGC ATT CTG GTG TTA ACA GTT CAG	959

Figure 8A

Phe Ile Leu Gly Trp Pro Leu Tyr Leu Ala Phe Asn Val Ser Gly Arg	202
TTT ATC CTC GGG TGG CCT TTG TAT CTA GCC TTT AAT GTA TCA GGT AGA	1007
Pro Tyr Asp Gly Phe Ala Ser His Phe Phe Pro His Ala Pro Ile Phe	218
CCT TAT GAT GGT TTC GCT TCA CAT TTC TTC CCT CAT GCA CCT ATC TTT	1055
Lys Asp Arg Glu Arg Leu Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu	234
AAA GAC CGA GAA CGC CTC CAG ATA TAC ATC TCA GAT GCT GGT ATT CTA	1103
Ala Val Cys Tyr Gly Leu Tyr Arg Tyr Ala Ala Ser Gln Gly Leu Thr	250
GCT GTC TGT TAT GGT CTT TAC CGT TAC GCT GCT TCA CAA GGA TTG ACT	1151
Ala Met Ile Cys Val Tyr Gly Val Pro Leu Leu Ile Val Asn Phe Phe	266
GCT ATG ATC TGC GTC TAT GGA GTA CCG CTT TTG ATA GTG AAC TTT TTC	1199
Leu Val Leu Val Thr Phe Leu Gln His Thr His Pro Ser Leu Pro His	282
CTT GTC TTG GTA ACT TTC TTG CAG CAC ACT CAT CCT TCG TTA CCT CAT	1247
Tyr Asp Ser Thr Glu Trp Glu Trp Ile Arg Gly Ala Leu Val Thr Val	298
TAT GAT TCA ACC GAG TGG GAA TGG ATT AGA GGA GCT TTG GTT ACG GTA	1295
Asp Arg Asp Tyr Gly Ile Leu Asn Lys Val Phe His Asn Ile Thr Asp	314
GAC AGA GAC TAT GGA ATA TTG AAC AAG GTG TTC CAT AAC ATA ACA GAC	1343
Thr His Val Ala His His Leu Phe Ala Thr Ile Pro His Tyr Asn Ala	330
ACA CAT GTG GCT CAT CAT CTC TTT GCA ACT ATA CCG CAT TAT AAC GCA	1391
Met Glu Ala Thr Glu Ala Ile Lys Pro Ile Leu Gly Asp Tyr Tyr His	346
ATG GAA GCT ACA GAG GCG ATA AAG CCA ATA CTT GGT GAT TAC TAC CAC	1439
Phe Asp Gly Thr Pro Trp Tyr Val Ala Met Tyr Arg Glu Ala Lys Glu	362
TTC GAT GGA ACA CCG TGG TAT GTG GCC ATG TAT AGG GAA GCA AAG GAG	1487
Cys Leu Tyr Val Glu Pro Asp Thr Glu Arg Gly Lys Lys Gly Val Tyr	378
TGT CTC TAT GTA GAA CCG GAT ACG GAA CGT GGG AAG AAA GGT GTC TAC	1535
Tyr Tyr Asn Asn Lys Leu	384
TAT TAC AAC AAT AAG TTA TGA GGC TGA TAG GGC GAG AGA AGT GCA ATT	1583
ATC AAT CTT CAT TTC CAT GTT TTA GGT GTC TTG TTT AAG AAG CTA TGC	1631
TTT GTT TCA ATA ATC TCA GAG TCC ATN TAG TTG TGT TCT GGT GCA TTT	1679
TGC CTA GTT ATG TGG TGT CGG AAG TTA GTG TTC AAA CTG CTT CCT GCT	1727
GTG CTG CCC AGT GAA GAA CAA GTT TAC GTG TTT AAA ATA CTC GGA ACG	1775
AAT TGA CCA CAA NAT ATC CAA AAC CGG CTA TCC GAA TTC CAT ATC CGA	1823
AAA CCG GAT ATC CAA ATT TCC AGA GTA CTT AG	1855

Figure 8B

		10	20	30	40	50	
LFFAH12	1	MGAGGRIM--	--VTPSSKKS	--ETEALKRG	PCEKPPFTVK	DLKKAIPQHC	50
FAH12	1	MGGGGRMSTV	ITSNNSEKKG	--GSSHLKRA	PHTKPPFTLG	DLKRAIPPHC	50
ATFAD2	1	MGAGGRMP--	--VPTSSKKS	--ETDTTKRV	PCEKPPFSVG	DLKKAIPPHC	50
BNFAD2	1	MGAGGRMQ--	--VSPPSKKS	--ETDNIKRV	PCETPPFTVG	ELKKAIPPHC	50
GMFAD2-1	1	MGLA-KETTM	GGRGRVAKVE	VQGKKPLSRV	PNTKPPFTVG	QLKKAIPPHC	50
GMFAD2-2	1	MGAGGR----	TDVPPANRKS	--EVDPLKRV	PFEKPPFSLS	QIKKAIPPHC	50
ZMFAD2	1	MGAGGRMTEK	EREKQEQLAR	ATGGAAMQRS	PVEKPPFTLG	QIKKAIPPHC	50
RCFAD2	1	-----	-----	-----	-----	-----	50
		60	70	80	90	100	
LFFAH12	51	FKRSIPRSFS	YLLTDITLVS	CFYYVATNYF	SLLPQPLSTY	LAWPLYWVCQ	100
FAH12	51	FERSFVRSFS	YVAYDVCLSF	LFYSIATNFF	PYISSPLS-Y	VAWLVIWLFQ	100
ATFAD2	51	FKRSIPRSFS	YLISDIIIAS	CFYYVATNYF	SLLPQPLS-Y	LAWPLYWACQ	100
BNFAD2	51	FKRSIPRSFS	HLIWDIIIAS	CFYYVATTYF	PLLPNPLS-Y	FAWPLYWACQ	100
GMFAD2-1	51	FQRSLLTSFS	YVVYDLSFAF	IFY-IATTYF	HLLPOPFS-L	IAWPIYWVLQ	100
GMFAD2-2	51	FQRSVLRSFS	YVVYDLTIAF	CLYYVATHYF	HLLPGPLS-F	RGMAIYWAVQ	100
ZMFAD2	51	FERSVLKSFS	YVVHDLVIAA	ALLYFALAI	PALPSPLR-Y	AAWPLYWIAQ	100
RCFAD2	51	-----	-----	-----	-----	-----	100
		110	120	130	140	150	
LFFAH12	101	GCVLTGIWVI	GHECGHHAFS	DYQWVDDTVG	FIFHSFLLVP	YFSWKYSHRR	150
FAH12	101	GCILTGLWVI	GHECGHHAFS	EYQLADDIVG	LIVHSALLVP	YFSWKYSHRR	150
ATFAD2	101	GCVLTGIWVI	AHECGHHAFS	DYQWLDDTVG	LIFHSFLLVP	YFSWKYSHRR	150
BNFAD2	101	GCVLTGVWVI	AHECGHAAFS	DYQWLDDTVG	LIFHSFLLVP	YFSWKYSHRR	150
GMFAD2-1	101	GCLLTGVWVI	AHECGHHAFS	KYQWVDDVVG	LTLHSTLLVP	YFSWKISHRR	150
GMFAD2-2	101	GCILTGVWVI	AHECGHHAFS	DYQLLDDIVG	LILHSALLVP	YFSWKYSHRR	150
ZMFAD2	101	G-----	-----AFS	DYSLDDDVVG	LVLHSSLMVP	YFSWKYSHRR	150
RCFAD2	101	-----WVM	AHDCGHHAFS	DYQLLDDVVG	LILHSCLLVP	YFSWKHSHRR	150
		160	170	180	190	200	
LFFAH12	151	HHSNNGSLEK	DEVFVPPKKA	AVKWYVKYL-	NNPLGRILVL	TVQFILGWPL	200
FAH12	151	HHSNIGSLER	DEVFVPKSKS	KISWYSKYS-	NNPPGRVLT	AATLLLGWPL	200
ATFAD2	151	HHSNTGSLER	DEVFVPKQKS	AIKWYGKYL-	NNPLGRIMML	TVQFVLGWPL	200
BNFAD2	151	HHSNTGSLER	DEVFVPR-RS	QTSSGSTAST-	STTFGRVMT	TVQFTLGWPL	200
GMFAD2-1	151	HHSNTGSLDR	DEVFVPKPKS	KVAWFSKYL-	NNPLGRAVSL	LVTLTIGWPM	200
GMFAD2-2	151	HHSNTGSLER	DEVFVPKQKS	CIKWYSKYL-	NNPPGRVLT	AVTLTLGWPL	200
ZMFAD2	151	HHSNTGSLER	DEVFVPKKKE	ALPWYTPYVY	NNPVGRVVHI	VVQLTLGWPL	200
RCFAD2	151	HHSNTGSLER	DEVFVPKKKS	SIRWYSKYL-	NNPPGRIMTI	AVTLSLGWPL	200
		210	220	230	240	250	
LFFAH12	201	YLAFNVSGRP	YDG-FASHFF	PHAPIFKDRE	RLQIYISDAG	ILAVCYGLYR	250
FAH12	201	YLAFNVSGRP	YDR-FACHYD	PYGPIFSERE	RLQIYIADLG	IFATTFVLYQ	250
ATFAD2	201	YLAFNVSGRP	YDG-FACHFF	PNAPIYNDRE	RLQIYLSDAG	ILAVCFGLYR	250
BNFAD2	201	YLAFNVSGRP	YDGGFACHFH	PNAPIYNDRE	RLQIYISDAG	ILAVCYGLLP	250
GMFAD2-1	201	YLAFNVSGRP	YDS-FASHYH	PYAPIYSNRE	RLLIYVSDVA	LFSVTYSLYR	250
GMFAD2-2	201	YLALNVSGRP	YDR-FACHYD	PYGPIYSDRE	RLQIYISDAG	VLAVVYGLFR	250
ZMFAD2	201	YLATNASGRP	YPR-FACHFD	PYGPIYNDRE	RAQIFVSDAG	VVAVAFGLYK	250
RCFAD2	201	YLAFNVSGRP	YDR-FACHYD	PYGPIYNDRE	RIEIFISDAG	VLAVTFGLYQ	250

Figure 9A

		260	270	280	290	300	
LFFAH12	251	YAASQGLTAM	ICVYGVPLLI	VNFFLVLVTF	LQHTHPSLPH	YDSTEWEWIR	300
FAH12	251	ATMAKGLAWV	MRIYGVPLLI	VNCFLVMITY	LQHTHPAIPR	YGSSEWDWLR	300
ATFAD2	251	YAAAQGMASM	ICLYGVPLLI	VNAFLVLITY	LQHTHPSLPH	YDSSEWDWLR	300
BNFAD2	251	YAAVQGVASM	VCFLRVPLLI	VNGFLVLITY	LQHTHPSLPH	YDSSEWDWLR	300
GMFAD2-1	251	VATLKGLVWL	LCVYGVPLLI	VNGFLVTITY	LQHTHFALPH	YDSSEWDWLK	300
GMFAD2-2	251	LAMAKGLAWV	VCVYGVPLLV	VNGFLVLITF	LQHTHPALPH	YTSSEWDWLR	300
ZMFAD2	251	LAAAFGVWWV	VRVYAVPLLI	VNAWLVLITY	LQHTHPSLPH	YDSSEWDWLR	300
RCFAD2	251	LATAKGLAWV	VCVYGVPLLV	VNSFLVLITF	LQHTHPALPH	YDSSEWDWLR	300
		310	320	330	340	350	
LFFAH12	301	GALVTVDRDY	GILNKVFHNI	TDTHVAHHLF	ATIPHYNAME	ATEAIKPILG	350
FAH12	301	GAMVTVDRDY	GVLNKVFHNI	ADTHVAHHLF	ATVPHYHAME	ATKAIKPIMG	350
ATFAD2	301	GALATVDRDY	GILNKVFHNI	TDTHVAHHLF	STMPHYNAME	ATKAIKPILG	350
BNFAD2	301	GALATVDRDY	GILNQGFHNI	TDTHEAHHLF	STMPHYHAME	ATKAIKPILG	350
GMFAD2-1	301	GALATMDRDY	GILNKVFHHI	TDTHVAHHLF	STMPHYHAME	ATNAIKPILG	350
GMFAD2-2	301	GALATVDRDY	GILNKVFHNI	TDTHVAHHLF	STMPHYHAME	ATKAIKPILG	350
ZMFAD2	301	GALATMDRDY	GILNRVFHNI	TDTHVAHHLF	STMPHYHAME	ATKAIRPILG	350
RCFAD2	301	GALATVDRDY	GILNKVFHNI	TDTOVAHHLF	-----	-----	350
		360	370	380	390	400	
LFFAH12	351	DYYHFDGTPW	YVAMYREAKE	CLYVEPDTER	GKKGVYYYNN	K-L.....	400
FAH12	351	EYYRYDGTPT	YKALWREAKE	CLFVEPDEGA	PTQGVFWYRN	KY-.....	400
ATFAD2	351	DYYQFDGTPW	YVAMYREAKE	CIYVEPDREG	DKKGVYWYNN	K-L.....	400
BNFAD2	351	EYYQFDGTPV	VKAMWREAKE	CIYVEPDROG	EKKGVFWYNN	KL*.....	400
GMFAD2-1	351	EYYQFDDTPF	YKALWREARE	CLYVEPDEGT	SEKGVYWYRN	KY-.....	400
GMFAD2-2	351	EYYRFDETPF	VKAMWREARE	CIYVEPDQST	ESKGVFWYNN	KL-.....	400
ZMFAD2	351	DYYHFDPTPV	AKATWREAGE	CIYVEPE---	DRKGVFWYNK	KF*.....	400

Figure 9B

09885189.062101

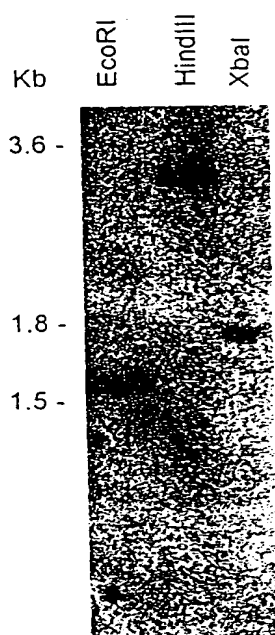
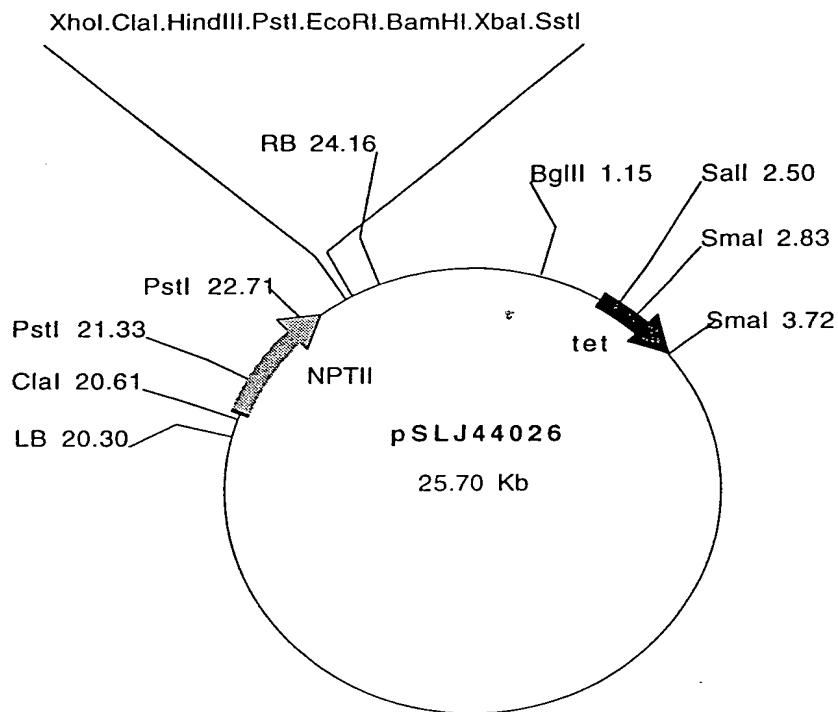


Figure 10

09885189-062101  
TOT290-68T58860



**Plasmid name:** pSLJ44026

**Plasmid size:** 25.70 kb

**Constructed by:** Jonathon Jones

**Construction date:** 1992

**Comments/References:** Transgenic Research 1,285-297 (1992)

**Figure 11**

0985189.062101  
TOT290" 68T58860

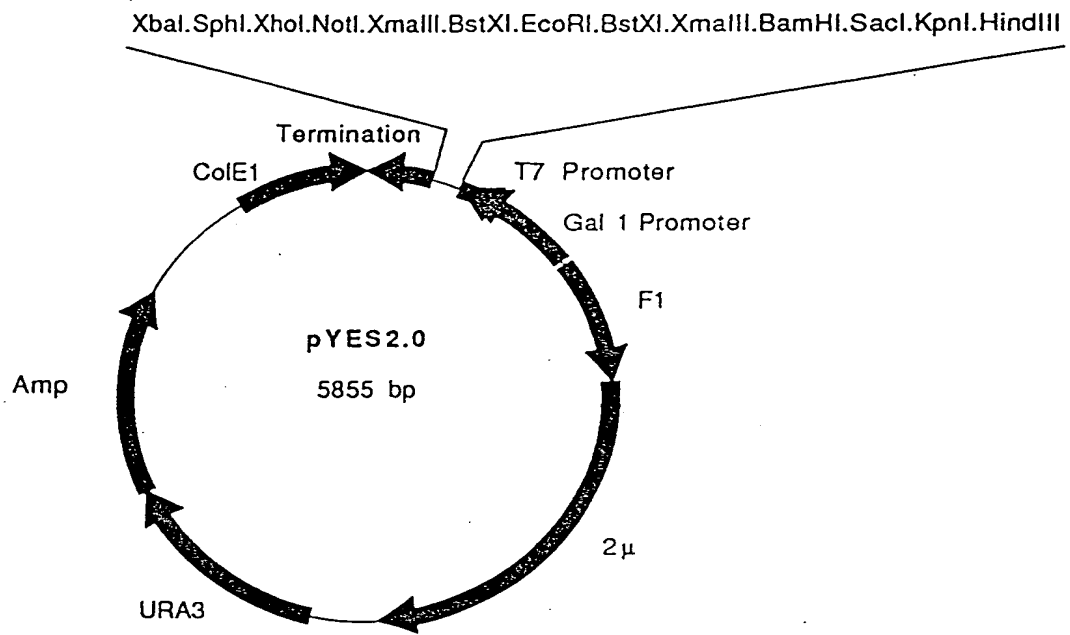


Figure 12



09:05:18.9-06:10.1  
T01290-68758660

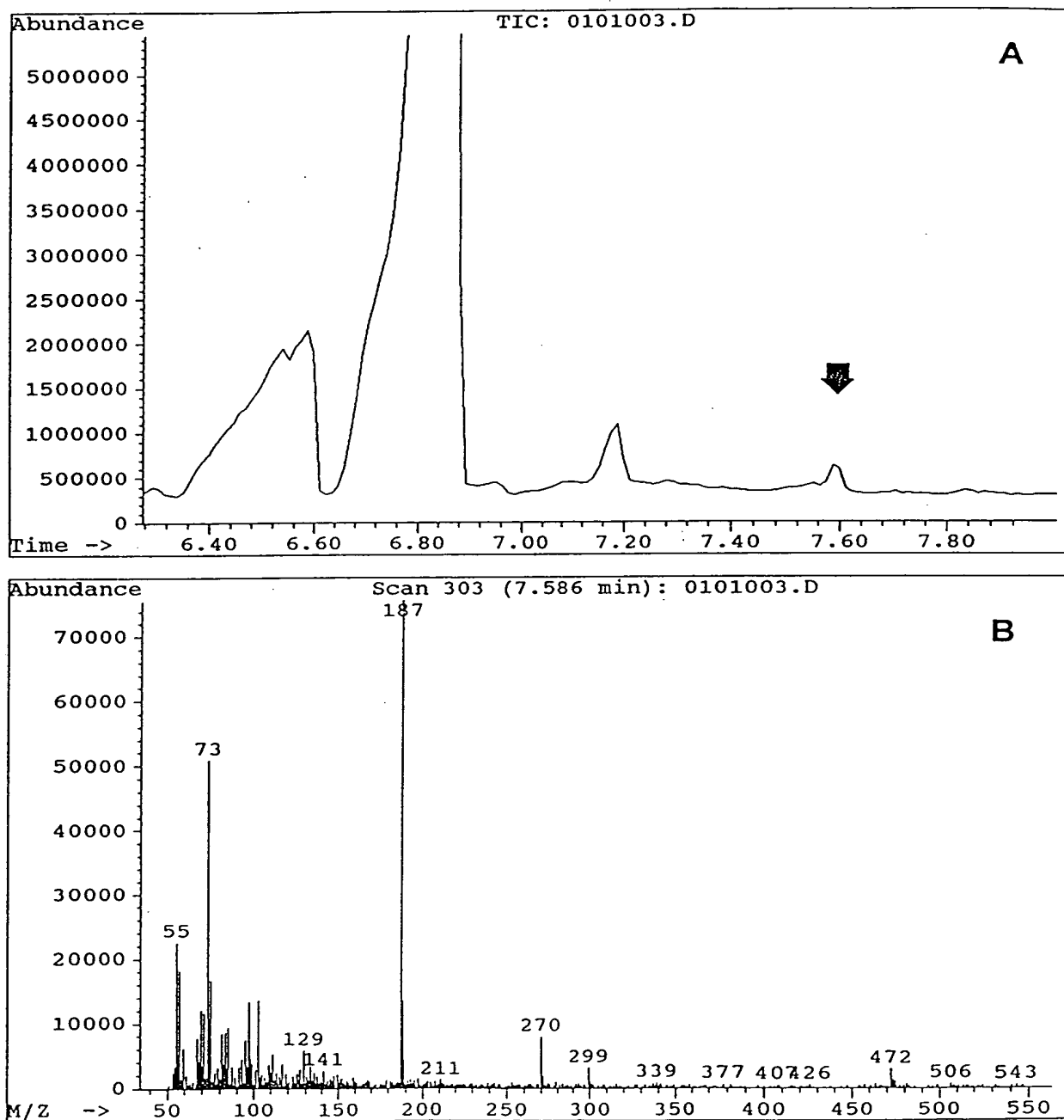


Figure 13